

SEQUENCE LISTING

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Lee, Jun

<120> Thermostable Reverse Transcriptases and Uses Thereof

<130> 0942.5040003

<150> US 60/410,283
<151> 2002-09-13

<160> 46

<170> PatentIn version 3.2

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<212> DNA
<213> Artificial Sequence

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Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Lys His
20 25 30

atg acc cta aat ata gaa gat gag tat cgg cta cat gag acc tca aaa 144
Met Thr Leu Asn Ile Glu Asp Glu Tyr Arg Leu His Glu Thr Ser Lys
35 40 45

gag cca gat gtt tct cta ggg tcc aca tgg ctg tct gat ttt cct cag 192
Glu Pro Asp Val Ser Leu Gly Ser Thr Trp Leu Ser Asp Phe Pro Gln
50 55 60

gcc tgg gcg gaa acc ggg ggc atg gga ctg gca gtt cgc caa gct cct 240
Ala Trp Ala Glu Thr Gly Met Gly Leu Ala Val Arg Gln Ala Pro
65 70 75 80

ctg atc ata ctt ctg aaa gca acc tct acc ccc gtg tcc ata aaa caa 288
Leu Ile Ile Leu Leu Lys Ala Thr Ser Thr Pro Val Ser Ile Lys Gln
85 90 95

tac ccc atg tca caa gaa gcc aga ctg ggg atc aag ccc cac ata cag 336
Tyr Pro Met Ser Gln Glu Ala Arg Leu Gly Ile Lys Pro His Ile Gln
100 105 110

aga ctg ttg gac cag gga ata ctg gta ccc tgc cag tcc ccc tgg aac	384
Arg Leu Leu Asp Gln Gly Ile Leu Val Pro Cys Gln Ser Pro Trp Asn	
115 120 125	
acg ccc ctg cta ccc gtc aag aaa ccc ggg act aat gat tac agg cct	432
Thr Pro Leu Leu Pro Val Lys Lys Pro Gly Thr Asn Asp Tyr Arg Pro	
130 135 140	
gtc caa gat ctg aga gag gtc aac aaa cgc gta gaa gac atc cac ccc	480
Val Gln Asp Leu Arg Glu Val Asn Lys Arg Val Glu Asp Ile His Pro	
145 150 155 160	
acc gta ccc aac ccc tac aac ctc ttg agt ggg ctc cca ccg tcc cac	528
Thr Val Pro Asn Pro Tyr Asn Leu Leu Ser Gly Leu Pro Pro Ser His	
165 170 175	
cag tgg tac act gtt cta gac tta aaa gat gcc ttt ttc tgc ctg aga	576
Gln Trp Tyr Thr Val Leu Asp Leu Lys Asp Ala Phe Phe Cys Leu Arg	
180 185 190	
ctc cac ccg acg tct cag cct ctc ttc gcc ttt gaa tgg aga gac cca	624
Leu His Pro Thr Ser Gln Pro Leu Phe Ala Phe Glu Trp Arg Asp Pro	
195 200 205	
gag atg gga atc tct ggc caa cta acc tgg acc aga ctc cca cag gga	672
Glu Met Gly Ile Ser Gly Gln Leu Thr Trp Thr Arg Leu Pro Gln Gly	
210 215 220	
ttc aaa aac agt ccc acc ctg ttt gat gag gca ctg cgc aga gac cta	720
Phe Lys Asn Ser Pro Thr Leu Phe Asp Glu Ala Leu Arg Arg Asp Leu	
225 230 235 240	
gca gac ttc cgg atc cag cac cca gac ttg atc ctg cta cag tac gta	768
Ala Asp Phe Arg Ile Gln His Pro Asp Leu Ile Leu Leu Gln Tyr Val	
245 250 255	
gat gac tta ctg ctg gcc act tct gag ctc gac tgc caa caa ggt	816
Asp Asp Leu Leu Ala Ala Thr Ser Glu Leu Asp Cys Gln Gln Gly	
260 265 270	
act cgg gcc ctg tta caa acc cta gga gac ctc ggg tat cgg gcc tcg	864
Thr Arg Ala Leu Leu Gln Thr Leu Gly Asp Leu Gly Tyr Arg Ala Ser	
275 280 285	
gcc aag aaa gcc caa att tgc cag aaa cag gtc aag tat ctg ggg tat	912
Ala Lys Lys Ala Gln Ile Cys Gln Lys Gln Val Lys Tyr Leu Gly Tyr	
290 295 300	
ctt cta aaa gag ggt cag aga tgg ctg act gag gcc aga aaa gag act	960
Leu Leu Lys Glu Gly Gln Arg Trp Leu Thr Glu Ala Arg Lys Glu Thr	
305 310 315 320	
gtg atg ggg cag cct act ccg aag acc ccg cgg caa cta agg gag ttc	1008
Val Met Gly Gln Pro Thr Pro Lys Thr Pro Arg Gln Leu Arg Glu Phe	
325 330 335	
cta ggg acg gca ggc ttc tgt cgc ctc tgg atc cct ggg ttt gca gaa	1056
Leu Gly Thr Ala Gly Phe Cys Arg Leu Trp Ile Pro Gly Phe Ala Glu	
340 345 350	
atg gca gcc ccc ttg tac cct ctc acc aaa acg ggg act ctg ttt aat	1104
Met Ala Ala Pro Leu Tyr Pro Leu Thr Lys Thr Gly Thr Leu Phe Asn	

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tgg ggc cca gac caa caa aag gcc tat caa gaa atc aag caa gct ctt Trp Gly Pro Asp Gln Gln Lys Ala Tyr Gln Glu Ile Lys Gln Ala Leu 370 375 380			1152
cta act gcc cca gcc ctg ggg ttg cca gat ttg act aag ccc ttt gaa Leu Thr Ala Pro Ala Leu Gly Leu Pro Asp Leu Thr Lys Pro Phe Glu 385 390 395 400			1200
ctc ttt gtc gac gag aag cag ggc tac gcc aaa ggt gtc cta acg caa Leu Phe Val Asp Glu Lys Gln Gly Tyr Ala Lys Gly Val Leu Thr Gln 405 410 415			1248
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att gcc gta ctg aca aag gat gca ggc aag cta acc atg gga cag cca Ile Ala Val Leu Thr Lys Asp Ala Gly Lys Leu Thr Met Gly Gln Pro 450 455 460			1392
cta gtc att ctg gcc ccc cat gca gta gag gca cta gtc aaa caa ccc Leu Val Ile Leu Ala Pro His Ala Val Glu Ala Leu Val Lys Gln Pro 465 470 475 480			1440
ccc gat cga tgg ctt tcc aac gcc cgg atg act cac tat cag gcc ttg Pro Asp Arg Trp Leu Ser Asn Ala Arg Met Thr His Tyr Gln Ala Leu 485 490 495			1488
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ccg gct aca ctg ctc cca ctg cct gag gaa ggg ctg cag cac aac tgc Pro Ala Thr Leu Leu Pro Leu Pro Glu Glu Gly Leu Gln His Asn Cys 515 520 525			1584
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aag aag cta aat gtt tat acg aat tcc cgt tat gct ttt gct act gcc	1872
Lys Lys Leu Asn Val Tyr Thr Asn Ser Arg Tyr Ala Phe Ala Thr Ala	
610 615 620	
cat atc cat gga gaa ata tac aga agg cgt ggg ttg ctc aca tca gaa	1920
His Ile His Gly Glu Ile Tyr Arg Arg Gly Leu Leu Thr Ser Glu	
625 630 635 640	
ggc aaa gag atc aaa aat aag gac gag ata ttg gcc cta cta aaa gcc	1968
Gly Lys Glu Ile Lys Asn Lys Asp Glu Ile Leu Ala Leu Leu Lys Ala	
645 650 655	
ctc ttt ctg ccc aaa aga ctt agc ata atc cat tgt cca gga cat caa	2016
Leu Phe Leu Pro Lys Arg Leu Ser Ile Ile His Cys Pro Gly His Gln	
660 665 670	
aag gga cac agc gcc gag gct aga ggc aac cgg atg gct gac caa gcg	2064
Lys Gly His Ser Ala Glu Ala Arg Gly Asn Arg Met Ala Asp Gln Ala	
675 680 685	
gcc cga aag gca gcc atc aca gag aat cca gac acc tct acc ctc ctc	2112
Ala Arg Lys Ala Ala Ile Thr Glu Asn Pro Asp Thr Ser Thr Leu Leu	
690 695 700	
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<223> Mutant Reverse Transcriptase Derived from Moloney Murine Leukemia Virus

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20 25 30	

Met Thr Leu Asn Ile Glu Asp Glu Tyr Arg Leu His Glu Thr Ser Lys	
35 40 45	

Glu Pro Asp Val Ser Leu Gly Ser Thr Trp Leu Ser Asp Phe Pro Gln	
50 55 60	

Ala Trp Ala Glu Thr Gly Gly Met Gly Leu Ala Val Arg Gln Ala Pro	
65 70 75 80	

Leu Ile Ile Leu Leu Lys Ala Thr Ser Thr Pro Val Ser Ile Lys Gln	
85 90 95	

Tyr Pro Met Ser Gln Glu Ala Arg Leu Gly Ile Lys Pro His Ile Gln
100 105 110

Arg Leu Leu Asp Gln Gly Ile Leu Val Pro Cys Gln Ser Pro Trp Asn
115 120 125

Thr Pro Leu Leu Pro Val Lys Lys Pro Gly Thr Asn Asp Tyr Arg Pro
130 135 140

Val Gln Asp Leu Arg Glu Val Asn Lys Arg Val Glu Asp Ile His Pro
145 150 155 160

Thr Val Pro Asn Pro Tyr Asn Leu Leu Ser Gly Leu Pro Pro Ser His
165 170 175

Gln Trp Tyr Thr Val Leu Asp Leu Lys Asp Ala Phe Phe Cys Leu Arg
180 185 190

Leu His Pro Thr Ser Gln Pro Leu Phe Ala Phe Glu Trp Arg Asp Pro
195 200 205

Glu Met Gly Ile Ser Gly Gln Leu Thr Trp Thr Arg Leu Pro Gln Gly
210 215 220

Phe Lys Asn Ser Pro Thr Leu Phe Asp Glu Ala Leu Arg Arg Asp Leu
225 230 235 240

Ala Asp Phe Arg Ile Gln His Pro Asp Leu Ile Leu Leu Gln Tyr Val
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Asp Asp Leu Leu Ala Ala Thr Ser Glu Leu Asp Cys Gln Gln Gly
260 265 270

Thr Arg Ala Leu Leu Gln Thr Leu Gly Asp Leu Gly Tyr Arg Ala Ser
275 280 285

Ala Lys Lys Ala Gln Ile Cys Gln Lys Gln Val Lys Tyr Leu Gly Tyr
290 295 300

Leu Leu Lys Glu Gly Gln Arg Trp Leu Thr Glu Ala Arg Lys Glu Thr
305 310 315 320

Val Met Gly Gln Pro Thr Pro Lys Thr Pro Arg Gln Leu Arg Glu Phe
325 330 335

Leu Gly Thr Ala Gly Phe Cys Arg Leu Trp Ile Pro Gly Phe Ala Glu

340

345

350

Met Ala Ala Pro Leu Tyr Pro Leu Thr Lys Thr Gly Thr Leu Phe Asn
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Trp Gly Pro Asp Gln Gln Lys Ala Tyr Gln Glu Ile Lys Gln Ala Leu
370 375 380

Leu Thr Ala Pro Ala Leu Gly Leu Pro Asp Leu Thr Lys Pro Phe Glu
385 390 395 400

Leu Phe Val Asp Glu Lys Gln Gly Tyr Ala Lys Gly Val Leu Thr Gln
405 410 415

Lys Leu Gly Pro Trp Arg Arg Pro Val Ala Tyr Leu Ser Lys Lys Leu
420 425 430

Asp Pro Val Ala Ala Gly Trp Pro Pro Cys Leu Arg Met Val Ala Ala
435 440 445

Ile Ala Val Leu Thr Lys Asp Ala Gly Lys Leu Thr Met Gly Gln Pro
450 455 460

Leu Val Ile Leu Ala Pro His Ala Val Glu Ala Leu Val Lys Gln Pro
465 470 475 480

Pro Asp Arg Trp Leu Ser Asn Ala Arg Met Thr His Tyr Gln Ala Leu
485 490 495

Leu Leu Asp Thr Asp Arg Val Gln Phe Gly Pro Val Val Ala Leu Asn
500 505 510

Pro Ala Thr Leu Leu Pro Leu Pro Glu Glu Gly Leu Gln His Asn Cys
515 520 525

Leu Asp Ile Leu Ala Glu Ala His Gly Thr Arg Pro Asp Leu Thr Asp
530 535 540

Gln Pro Leu Pro Asp Ala Asp His Thr Trp Tyr Thr Gly Gly Ser Ser
545 550 555 560

Leu Leu Gln Glu Gly Gln Arg Lys Ala Gly Ala Ala Val Thr Thr Glu
565 570 575

Thr Glu Val Ile Trp Ala Lys Ala Leu Pro Ala Gly Thr Ser Ala Gln
580 585 590

Arg Ala Gln Leu Ile Ala Leu Thr Gln Ala Leu Arg Met Ala Glu Gly
595 600 605

Lys Lys Leu Asn Val Tyr Thr Asn Ser Arg Tyr Ala Phe Ala Thr Ala
610 615 620

His Ile His Gly Glu Ile Tyr Arg Arg Gly Leu Leu Thr Ser Glu
625 630 635 640

Gly Lys Glu Ile Lys Asn Lys Asp Glu Ile Leu Ala Leu Leu Lys Ala
645 650 655

Leu Phe Leu Pro Lys Arg Leu Ser Ile Ile His Cys Pro Gly His Gln
660 665 670

Lys Gly His Ser Ala Glu Ala Arg Gly Asn Arg Met Ala Asp Gln Ala
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Ala Arg Lys Ala Ala Ile Thr Glu Asn Pro Asp Thr Ser Thr Leu Leu
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Ile Glu Asn Ser Ser Pro Asn Ser Arg Leu Ile Asn
705 710 715

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Ile Glu Gly Arg
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Leu Val Pro Arg
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gctaysacca tgattacgns caagcytgca tgcctgcagg tcgactctag aggatccccg 180
ggtaccgagc tcgaattyac tggycgtcgt tntwacaacg tcgtgwctgg gaanaaccct 240
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agcg 304

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Asp Asp Asp Lys
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